

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 240 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20 and 22, or a second nucleotide sequence comprising the complement of the first nucleotide sequence.
2. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19 and 21 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20 and 22.
3. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are DNA.
4. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are RNA.
5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.
6. An isolated host cell comprising the chimeric gene of Claim 5.
7. A host cell comprising an isolated polynucleotide of Claim 1.
8. The host cell of Claim 7 wherein the host cell is selected from the group consisting of yeast, bacteria, plant, and virus.
9. A virus comprising the isolated polynucleotide of Claim 1.
10. A polypeptide of at least 240 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20 and 22.
11. A method of selecting an isolated polynucleotide that affects the level of expression of a carbon catabolite repression polypeptide in a plant cell, the method comprising the steps of:
  - (a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from an isolated polynucleotide of Claim 1;
  - (b) introducing the isolated polynucleotide into a plant cell;
  - (c) measuring the level of a polypeptide in the plant cell containing the polynucleotide to provide a positive selection means.
12. The method of Claim 11 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19 and 21 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20 and 22.

13. A method of selecting an isolated polynucleotide that affects the level of expression of a carbon catabolite repression polypeptide in a plant cell, the method comprising the steps of:

- 5 (a) constructing an isolated polynucleotide of Claim 1;  
(b) introducing the isolated polynucleotide into a plant cell; and  
(c) measuring the level of polypeptide in the plant cell containing the polynucleotide to provide a positive selection means.

14. A method of obtaining a nucleic acid fragment encoding a carbon catabolite repression polypeptide comprising the steps of:

- 10 (a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such nucleotide sequences; and

(b) amplifying a nucleic acid sequence using the oligonucleotide primer.

15 15. A method of obtaining a nucleic acid fragment encoding a carbon catabolite repression polypeptide comprising the steps of:

- 20 (a) probing a cDNA or genomic library with an isolated polynucleotide comprising at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such nucleotide sequences;  
(b) identifying a DNA clone that hybridizes with the isolated polynucleotide;  
(c) isolating the identified DNA clone; and  
(d) sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.

25 16. A composition comprising the isolated polynucleotide of Claim 1.

17. An isolated polynucleotide comprising the nucleotide sequence having at least one of 30 contiguous nucleotides derived from a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such sequences.

30 18. An expression cassette comprising an isolated polynucleotide of Claim 1 operably linked to a promoter.

19. A method for positive selection of a transformed cell comprising:

- 35 (a) transforming a host cell with the chimeric gene of Claim 5 or an expression cassette of Claim 18; and  
(b) growing the transformed host cell under conditions which allow expression of the polynucleotide in an amount sufficient to alter expression of glucose repressible genes to provide a positive selection means.

20. The method of Claim 19 wherein the host is a plant cell.

21 The method of Claim 19 wherein the plant cell is a dicot or a monocot.

22. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 77 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of  
5 SEQ ID NOs:24, 26 and 28, or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

23. A polypeptide of at least 77 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:24, 26 and 28, or a second nucleotide sequence comprising the  
10 complement of the first nucleotide sequence.